

Reviewer Report

Title: Genome Diversity in Ukraine

Version: Revision 1 **Date:** 9/14/2020

Reviewer name: Chaochun Wei

Reviewer Comments to Author:

This paper reported 97 whole sequencing data of representative Ukrainians and their variation annotations using DNBSEQ-G50 sequencing platform. Illumina NovaSeq6000 S4 sequencing for one individual was done as quality control of sequencing. Genomic variants including SVs, indels, CNVs, SNPs and microsatellites were annotated and compared to neighboring populations. The goal of this paper is to provide a genomic resource for Eastern Europe. A few issues are listed below.

Major issues

1. Accession numbers or IDs for all data are not provided yet.
2. In Table S2, the number of SNPs, filtered counts and percentage filtered has no value.
3. Will the sequencing depth impact the assembled genomes? For example, the illumine sequencing depth was 60 while DNBSEQ-G50 sequencing data have about 30X coverage.
4. In the first paragraph of page 14, the authors mentioned that "genetics is not a reliable determinant of ethnicity", this is conclusion is not well supported with evidences. Another explanation can be that the self-identified ethnic group is not reliable.

Minor issues

1. There are some language issues. For example, in the first paragraph of Page 4, "while the ethnic Ukrainians constitute approximately than three quarters of the total population of the modern Ukraine". "than" in this sentence should be removed.

Level of Interest

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